

SEQUENCE LISTING

<110> Taylor, J. Michael
Kehrli, Jr., Marcus
Lee, Eun-Kyung
Mwangi, Simon

<120> BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
AND METHODS OF USE

<130> 08411-018001

<140> 09/513,007

<141> 2000-02-25

<150> 60/122,156

<151> 1999-02-26

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2440

<212> DNA

<213> Bos taurus

<220>

<221> CDS

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gacccgaggc	ccgggctcca	ctgggcatac	gcgaggaccg	tggtgctgtc	actgtcgcgg	240
gccgccactg	ccccagccct	gatgggggat	tgagaggcca	cagctggccg	gac atg	296
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				1		

ggc ctc ccc acc gtg cct ggc ctg ctg ctg cca ctg gtg ctt cca gct	344
Gly Leu Pro Thr Val Pro Gly Leu Leu Leu Pro Leu Val Leu Pro Ala	
5 10 15	

ctg ttg gca gat gtg tac ccc gca ggg gtt cag ggg ctg gtc cct cac	392
Leu Leu Ala Asp Val Tyr Pro Ala Gly Val Gln Gly Leu Val Pro His	
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ccc ggg gac ctg gag aag aga gag agt ccc tgt ccc caa gga aaa tat	440
Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro Gln Gly Lys Tyr	
35 40 45	

aac cac ccg caa aat agc acc att tgc tgc acc aag tgc cac aaa ggt	488
Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys Cys His Lys Gly	
50 55 60 65	

acc tat ctg tac aat gac tgt ccg ggt cca ggg cga gac acg gac tgc	536
Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg Asp Thr Asp Cys	
70 75 80	

0997052-100201

agg gtg tgt gcc cct ggc acc tac act gcc ttg gag aac cat ctc aga	584
Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu Asn His Leu Arg	
85 90 95	
cga tgc ctg agc tgc tcc agg tgc cgg gac gaa atg ttc cag gtg gag	632
Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met Phe Gln Val Glu	
100 105 110	
att tcg cct tgt gta gtg gac cgg gac act gtg tgc ggc tgc agg aag	680
Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys	
115 120 125	
aac cag tac cgg gaa tac tgg ggt gaa act ggc ttc cgg tgt ctg aac	728
Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe Arg Cys Leu Asn	
130 135 140 145	
tgc agc ctc tgt ccc aat ggc aca gtg aat atc ccc tgc cag gag aga	776
Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro Cys Gln Glu Arg	
150 155 160	
cag gac acc atc tgc cac tgc cat atg ggc ttc ttt ctt aaa ggc gcc	824
Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe Leu Lys Gly Ala	
165 170 175	
aag tgc atc tcc tgt cat gat tgt aag aac aag gag tgc gag aag tta	872
Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu Cys Glu Lys Leu	
180 185 190	
tgt cca acc cga cct tca act ggt aaa gac tct cag gac cca ggc act	920
Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln Asp Pro Gly Thr	
195 200 205	
aca gta cta tta ccc ctg gtg att gtc ttc ggg ctt tgc ctg gca tcc	968
Thr Val Leu Leu Pro Leu Val Ile Val Phe Gly Leu Cys Leu Ala Ser	
210 215 220 225	
ttc gcc tct gtc gtc tta gca tgt cgc tac cag cgg tgg aag ccc aag	1016
Phe Ala Ser Val Val Leu Ala Cys Arg Tyr Gln Arg Trp Lys Pro Lys	
230 235 240	
ctc tac tcc atc att tgc ggg cag tgc act ctg gta aaa gag ggg gag	1064
Leu Tyr Ser Ile Ile Cys Gly Gln Ser Thr Leu Val Lys Glu Gly Glu	
245 250 255	
cca gaa ctc ctg gtc ccg gcc cca ggc ttc aac ccc acc acc acc atc	1112
Pro Glu Leu Leu Val Pro Ala Pro Gly Phe Asn Pro Thr Thr Thr Ile	
260 265 270	
tgc ttc agc tcc acc cca agt tcc agt cct gtc tcc att ccc cct tac	1160
Cys Phe Ser Ser Thr Pro Ser Ser Ser Pro Val Ser Ile Pro Pro Tyr	
275 280 285	
atc tcc tgt gac cgg tcc aac ttc gga gcc gtc gca tct ccc tcc agc	1208
Ile Ser Cys Asp Arg Ser Asn Phe Gly Ala Val Ala Ser Pro Ser Ser	
290 295 300 305	
gag acg gcc ccg ccc cat cta aag gct ggc ccc atc ctc ccg ggg cct	1256
Glu Thr Ala Pro Pro His Leu Lys Ala Gly Pro Ile Leu Pro Gly Pro	
310 315 320	
ccg gcc tcc acc cac ctc tgt acc ccg ggg cct ccg gcc tcc acc cac	1304

T0200T-2E502660

Pro Ala Ser Thr His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His
325 330 335

ctc tgt acc ccg ggg cct ccg gcc tcc acc cac ctc tgc acc cca gtt 1352
Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His Leu Cys Thr Pro Val
340 345 350

cag aag tgg gaa gcc agc gcc ccc agc gcc ccc gat cag ctc gcg gat 1400
Gln Lys Trp Glu Ala Ser Ala Pro Ser Ala Pro Asp Gln Leu Ala Asp
355 360 365

gcc gac ccc gcg acc ctg tac gcg gtg gtg gac gcc gtg ccc ccg tcg 1448
Ala Asp Pro Ala Thr Leu Tyr Ala Val Val Asp Gly Val Pro Pro Ser
370 375 380 385

cgc tgg aag gag ttg gtg cgg cgg ctg gga ctg agc gag cac gag atc 1496
Arg Trp Lys Glu Leu Val Arg Arg Leu Gly Leu Ser Glu His Glu Ile
390 395 400

gag cgg ctg gag ctg gag aac ggg cgc cac ctg cgc gag gcg cag tac 1544
Glu Arg Leu Glu Leu Glu Asn Gly Arg His Leu Arg Glu Ala Gln Tyr
405 410 415

agc atg ctg gcg gcc tgg cgg cgg cgc acg ccg cgc cgc gag gcc acg 1592
Ser Met Leu Ala Ala Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr
420 425 430

ctg gag ctg ctg gcc cgc gtg ctc agg gac atg gac ctg ctg ggt tgc 1640
Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys
435 440 445

ctg gaa aac ata gag gag gcg ctg ggt gcc gcc gcc cgc ctc gcg tcc 1688
Leu Glu Asn Ile Glu Glu Ala Leu Gly Gly Ala Ala Arg Leu Ala Ser
450 455 460 465

gag ccc cgc ctt ctc tgg tgaagccccg cccctccgac tgcgggcctc 1736
Glu Pro Arg Leu Leu Trp
470

cccgccctgc agacggtgc ttccttctgc tgccaggcag cccggaagga tctgcgagat 1796
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<211> 471

<212> PRT

<213> Bos taurus

<400> 2

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T0001-2502650

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 His Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro Gln Gly Lys
 35 40 45
 Tyr Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys Cys His Lys
 50 55 60
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg Asp Thr Asp
 65 70 75 80
 Cys Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu Asn His Leu
 85 90 95
 Arg Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met Phe Gln Val
 100 105 110
 Glu Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 115 120 125
 Lys Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe Arg Cys Leu
 130 135 140
 Asn Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro Cys Gln Glu
 145 150 155 160
 Arg Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe Leu Lys Gly
 165 170 175
 Ala Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu Cys Glu Lys
 180 185 190
 Leu Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln Asp Pro Gly
 195 200 205
 Thr Thr Val Leu Leu Pro Leu Val Ile Val Phe Gly Leu Cys Leu Ala
 210 215 220
 Ser Phe Ala Ser Val Val Leu Ala Cys Arg Tyr Gln Arg Trp Lys Pro
 225 230 235 240
 Lys Leu Tyr Ser Ile Ile Cys Gly Gln Ser Thr Leu Val Lys Glu Gly
 245 250 255
 Glu Pro Glu Leu Leu Val Pro Ala Pro Gly Phe Asn Pro Thr Thr Thr
 260 265 270
 Ile Cys Phe Ser Ser Thr Pro Ser Ser Ser Pro Val Ser Ile Pro Pro
 275 280 285
 Tyr Ile Ser Cys Asp Arg Ser Asn Phe Gly Ala Val Ala Ser Pro Ser
 290 295 300
 Ser Glu Thr Ala Pro Pro His Leu Lys Ala Gly Pro Ile Leu Pro Gly
 305 310 315 320
 Pro Pro Ala Ser Thr His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr
 325 330 335
 His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His Leu Cys Thr Pro
 340 345 350
 Val Gln Lys Trp Glu Ala Ser Ala Pro Ser Ala Pro Asp Gln Leu Ala
 355 360 365
 Asp Ala Asp Pro Ala Thr Leu Tyr Ala Val Val Asp Gly Val Pro Pro
 370 375 380
 Ser Arg Trp Lys Glu Leu Val Arg Arg Leu Gly Leu Ser Glu His Glu
 385 390 395 400
 Ile Glu Arg Leu Glu Leu Glu Asn Gly Arg His Leu Arg Glu Ala Gln
 405 410 415
 Tyr Ser Met Leu Ala Ala Trp Arg Arg Thr Pro Arg Arg Glu Ala
 420 425 430
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
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 Cys Leu Glu Asn Ile Glu Glu Ala Leu Gly Gly Ala Ala Arg Leu Ala
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 Ser Glu Pro Arg Leu Leu Trp
 465 470

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<211> 543

<212> DNA

T0001-22502660

<213> Bos taurus

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 Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg
 35 40 45
 Asp Thr Asp Cys Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu
 50 55 60
 Asn His Leu Arg Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met
 65 70 75 80
 Phe Gln Val Glu Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys
 85 90 95
 Gly Cys Arg Lys Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe
 100 105 110
 Arg Cys Leu Asn Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro
 115 120 125
 Cys Gln Glu Arg Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe
 130 135 140
 Leu Lys Gly Ala Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu
 145 150 155 160
 Cys Glu Lys Leu Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln
 165 170 175
 Asp Pro Gly Thr Thr
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<210> 6
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 <212> DNA
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 <212> DNA
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<220>
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<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide for PCR

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